1600

RAW SEQUENCE LISTING   DATE: 06/05/2003
PATENT APPLICATION: US/09/068,507B   TIME: 13:44:51

Input Set : A:\2003-05-30 1380-0122P.ST25.txt
Output Set: N:\CRF4\06052003\I068507B.raw

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    3 <110> APPLICANT: EIJSINK, VINCENT et al.
    5 <120> TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND ITS USE FOR
EXPRESSING
    6       HETEROLOGOUS AND HOMOLOGOUS PROTEINS
    8 <130> FILE REFERENCE: 1380-0122P
   10 <140> CURRENT APPLICATION NUMBER: US 09/068,507B
C--> 11 <141> CURRENT FILING DATE: 1998-07-18
   13 <160> NUMBER OF SEQ ID NOS: 19
   15 <170> SOFTWARE: PatentIn version 3.1
   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 26
   19 <212> TYPE: PRT
   20 <213> ORGANISM: Lactobacillus plantarum
   22 <400> SEQUENCE: 1
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   29             20                  25
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   33 <211> LENGTH: 114
   34 <212> TYPE: DNA
   35 <213> ORGANISM: Lactobacillus sake
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   40 <223> OTHER INFORMATION:
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   45 1               5                   10                  15
   47 ggt ggt atg gca gga aat agt tct aat ttt att cat aag att aaa caa      96
   48 Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
   49             20                  25                  30
   51 att ttt acc cat cgt taa                                              114
   52 Ile Phe Thr His Arg
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   58 <212> TYPE: PRT
   59 <213> ORGANISM: Lactobacillus sake
   61 <400> SEQUENCE: 3
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  71 Ile Phe Thr His Arg
  72         35
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  83 <223> OTHER INFORMATION:
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  87 Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
  88 1               5               10              15
  90 ggt gga aaa tat tat ggt aac ggt gta cac tgt gga aaa cat tca tgt        96
  91 Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
  92         20              25              30
  94 acc gta gac tgg gga aca gct att gga aat atc gga aat aat gca gct       144
  95 Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
  96         35              40              45
  98 gca aac tgg gcc aca ggc gga aac gct ggc tgg aat aaa taa              186
  99 Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys
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 104 <211> LENGTH: 61
 105 <212> TYPE: PRT
 106 <213> ORGANISM: Lactobacillus sake
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 110 Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
 111 1               5               10              15
 114 Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
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 118 Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
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 127 <211> LENGTH: 81
 128 <212> TYPE: DNA
 129 <213> ORGANISM: Lactobacillus sake
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 134 tgaattatgt ataaatttgat t                                              81
 137 <210> SEQ ID NO: 7
 138 <211> LENGTH: 80
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 140 <213> ORGANISM: Lactobacillus sake
 142 <400> SEQUENCE: 7
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Input Set : **A:\2003-05-30 1380-0122P.ST25.txt**
Output Set: **N:\CRF4\06052003\I068507B.raw**

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143 cgcatattaa cgtttaaccg ataaagttga acgttaatat ttttttttgcg cagaaatggt     60
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151 <213> ORGANISM: Lactobacillus sake
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160 <211> LENGTH: 81
161 <212> TYPE: DNA
162 <213> ORGANISM: Lactobacillus sake
164 <400> SEQUENCE: 9
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167 gatttgaagc ataatggtgt t                                                 81
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171 <211> LENGTH: 81
172 <212> TYPE: DNA
173 <213> ORGANISM: Lactobacillus plantarum
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183 <212> TYPE: DNA
184 <213> ORGANISM: Staphylococcus aureus
186 <400> SEQUENCE: 11
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189 actaaatcgt ataatgacag                                                   80
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234 <223> OTHER INFORMATION: gene="sppR"
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240 <220> FEATURE:
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242 <222> LOCATION: (2736)..(2741)
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (2813)..(2998)
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272 <222> LOCATION: (3675)..(3680)
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276 <222> LOCATION: (3739)..(5895)
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289 <222> LOCATION: (5910)..(7286)
290 <223> OTHER INFORMATION: gene="sppE"
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295 tgaattttac caaagccaac actataaata taatttgcga ggcggttgac taacacttca     120
297 ggattcttgg cagtttcaag tgtgagatag acctgactca aaacatcggt aatgtcgaga     180
299 agcgcgtttg atttatctgg atgagccatt aggctgttgt aaagtgtatg aatgttttcc     240
301 ttagcaattt cttgattagt cataatgaaa agcctccaca aaaagtatta tcaacatctg     300
303 ttctagtctt cttagtaaat tttgtcaact tcaatagagt tcttaacgtt aatccgaaaa     360
305 aaactaacgt taatattaaa aaataagatc cgcttgtgaa ttatgtataa tttgattaga     420
307 ctaaagaata ggagaaagta tgatgatatt taaaaaactt tcagaaaaag aattgcaaaa     480
309 aataaacggt ggtatggcag gaaatagttc taattttatt cataagatta aacaaatttt     540
311 tacccatcgt taagataggt tgttggtgag c atg tta tat acg gat gta tcg       592
312                                   Met Leu Tyr Thr Asp Val Ser
313                                    1               5
315 gtt tcc tta atg caa aat ttt gtt gct atc tta tta att ttt cta tta     640
316 Val Ser Leu Met Gln Asn Phe Val Ala Ile Leu Leu Ile Phe Leu Leu
317         10              15                  20
319 tat aga tat att caa aga aag ata aca ttt aaa cgg atc ata tta gat     688
320 Tyr Arg Tyr Ile Gln Arg Lys Ile Thr Phe Lys Arg Ile Ile Leu Asp
321     25              30                  35
323 att tta ata gcg att att ttt tca ata tta tat ctg ttt att tca gat     736
324 Ile Leu Ile Ala Ile Ile Phe Ser Ile Leu Tyr Leu Phe Ile Ser Asp
325 40              45                  50                  55
327 gcg tca tta ctt gta atg gta tta atg cga tta ggg tgg cat ttt cat     784
328 Ala Ser Leu Leu Val Met Val Leu Met Arg Leu Gly Trp His Phe His
329                 60                  65                  70
331 caa caa aaa gaa aat aag ata aaa acg act gat aca gct aat tta att     832
332 Gln Gln Lys Glu Asn Lys Ile Lys Thr Thr Asp Thr Ala Asn Leu Ile
333             75                  80                  85
335 cta att atc gtg atc cag tta ttg tta gtt gcg gtt ggg act att att     880
336 Leu Ile Ile Val Ile Gln Leu Leu Leu Val Ala Val Gly Thr Ile Ile
337             90                  95                  100
339 agt cag ttt acc ata tcg att atc aaa agt gat ttc agc caa aat ata     928
340 Ser Gln Phe Thr Ile Ser Ile Ile Lys Ser Asp Phe Ser Gln Asn Ile
341     105                 110                 115
343 ttg aac aat agt gca aca gat ata act tta tta ggt att ttc ttt gct     976
344 Leu Asn Asn Ser Ala Thr Asp Ile Thr Leu Leu Gly Ile Phe Phe Ala
345 120                 125                 130                 135
347 gtt tta ttt gac ggc ttg ttc ttt ata tta ttg aag aat aag cgg act    1024
348 Val Leu Phe Asp Gly Leu Phe Phe Ile Leu Leu Lys Asn Lys Arg Thr
349                 140                 145                 150
351 gaa tta caa cat tta aat caa gaa atc att gaa ttt tcg tta gaa aaa    1072
352 Glu Leu Gln His Leu Asn Gln Glu Ile Ile Glu Phe Ser Leu Glu Lys
353             155                 160                 165
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VERIFICATION SUMMARY
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:40
L:85 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:83